

KLW

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,267

DATE: 07/27/2001

TIME: 19:01:22

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07272001\I889267.raw

ENTERED

4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: NEISSERIA MENINGITIDIS ANTIGEN
9 <130> FILE REFERENCE: BM45351
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/889,267
C--> 11 <141> CURRENT FILING DATE: 2001-07-13
11 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00137
12 <151> PRIOR FILING DATE: 2000-01-10
14 <160> NUMBER OF SEQ ID NOS: 6
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2169
20 <212> TYPE: DNA
21 <213> ORGANISM: Neisseria meningitidis
23 <400> SEQUENCE: 1
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25 ctttcgtctt cggtttttgc cgcacaaacg gcggatttgg aaaccgtcca catcaaaggg 120
26 cagcgttcgt acaacgcgat tgtcaccgag aaaaacggcg attacagctc gtttgccgtc 180
27 accgtcggca caaaaatccc cgcttctttg cgcgaaattc cgcaatccgt cagtatcatc 240
28 accaaccagc aggtcaaaga ccgcaatggt gatacgtttg accagttggc gcgcaaaacg 300
29 cccggcctgc gcgtgttgag caacgatgac ggacgctctt cggtttacgc gcgcggttac 360
30 gaatacagcg aatacaacat cgacggcctg cccgcgcaga tgcagagtat caacggcacg 420
31 ctgcccaatc tgttgcgctt cgaccgcgtg gaagtgatgc gcgggcccag cggactgttc 480
32 gacagcagcg gcgagatggg cggtatcgtg aatctggtgc gcaaacgccc gaccaaaagcg 540
33 ttccaaggctc atgctgcggc agggttcggg acgcacaaac aatataaagc cgaggcggac 600
34 gtatcgggca gcctcaattc agacggcagc gtgcgcggcc gcgtgatggc gcagaccgtc 660
35 ggcgcgtctc cgcgtcccgc cgagaaaaac aaccggcacg aaaccttcta cgcggcggcg 720
36 gattgggaca tcaaccccga tacggttttg ggcgcgggct atctttacca gcaacgcca 780
37 ctgcgcgctt acaacggctt gccagcgcgt gccataaaca aattaccgtc cctgccgcaa 840
38 cactgtattg tcggcgcgga ttggaacaaa tttaaaatga acagccacga cgtgtttgcc 900
39 gatttgaaac attacttcgg caacggcggc tacggcaaaag tcggtatgcy ctattccgac 960
40 cgcgatgccg actccaacta tgcctttgcc ggcagcaagc tgggcatgaa aaccccggca 1020
41 ggccgcccgg gctgcaatac ggctgacgac aaagcctgcg cggtggtttt gggtagagaa 1080
42 atcaaacaaa aagccctcgc gtttgacgcc agctacagca ggccctttccg cttgggcaat 1140
43 acggccaacg aatttgtcat cggcgccgat tacaaccgct tccgcagcac caacgaacaa 1200
44 ggccgtacta ctttatatgc acgcggcggc ctggctttta acgagttccg cagcataccg 1260
45 caggttgatt tgattgcaa cgcgcgcaaa ggctgcgcg gttacagcca taccgtcgtc 1320
46 accgaaaacc tcgacgaatt cggcatttac ggcaaatcca ccttccatcc tgccgacggg 1380
47 ctgtcgcctt tcggcgggcg acgtttggga cactataaaa tcgagtcggg cgaaggcaaa 1440
48 accctgcaca aagccagcaa aaccaagttc accggctacg caggcgcggt ttacgacttg 1500
49 aacgacaaca acagcctcta cctgagcctg tcccagctct acacaccgca aaccaacctc 1560
50 gatgccgacg gcaagctgct caaacgcgc caaggcaacc agtttgaagt cggttacaaa 1620
51 ggcagctaca tggacgaccg cctcaatgcc cgagtttcgt tctaccgcat gaaagacaaa 1680
52 aacggcggcg caccgttgaa cccgaacaac aaaaaaaccc gttacggcgc attgggcaaa 1740
53 cgcgtgatgg aaggcgttga gaccgaaatc agcggcgcgg ttacaccgaa atggcaaatc 1800
54 catgcaggtt acagctatct gcacagccaa atcaaaaccg cctccaattc acgcgacgac 1860
55 ggcatacttc tgctgatgcc caaacacagc gccaaacctg ggacgactta ccaagttacg 1920
56 cccgagctga ccatcgggcg cggagtgaac gcgatgagcg gcattacttc atctgcaggg 1980

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57 atgcatgcag gcggttatgc cacgttcgat gcgatggcgg cataccgctt cagcccaag      2040
58 ctgaagctgc aaatcaacgc cgacaacatc ttcaaccgcc attactacgc ccgcgtcggc      2100
59 ggcggaaca cctttaacat tcccggttcg gagcgcacct ggacggcaaa cctgcgttac      2160
60 agtttttaa                                     2169
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 722
64 <212> TYPE: PRT
65 <213> ORGANISM: Neisseria meningitidis
67 <400> SEQUENCE: 2
68 Met Gly Gln Phe Met Ser Val Phe Arg Ile Asn Met Thr Ala Ala Thr
69 1 5 10 15
70 Val Leu Ala Ala Leu Ser Ser Ser Val Phe Ala Ala Gln Thr Ala Asp
71 20 25 30
72 Leu Glu Thr Val His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile Val
73 35 40 45
74 Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly Thr
75 50 55 60
76 Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile Ile
77 65 70 75 80
78 Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln Leu
79 85 90 95
80 Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly Arg
81 100 105 110
82 Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile Asp
83 115 120 125
84 Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn Leu
85 130 135 140
86 Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu Phe
87 145 150 155 160
88 Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys Arg
89 165 170 175
90 Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr His
91 180 185 190
92 Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser Asp
93 195 200 205
94 Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser Pro
95 210 215 220
96 Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala Ala
97 225 230 235 240
98 Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu Tyr
99 245 250 255
100 Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala Asn
101 260 265 270
102 Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp Trp
103 275 280 285
104 Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys His
105 290 295 300
106 Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser Asp
107 305 310 315 320

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108 Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly Met
109           325           330           335
110 Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys Ala
111           340           345           350
112 Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala Phe
113           355           360           365
114 Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn Glu
115           370           375           380
116 Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu Gln
117 385           390           395           400
118 Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu Phe
119           405           410           415
120 Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly Val
121           420           425           430
122 Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe Gly
123           435           440           445
124 Ile Tyr Gly Lys Ser Thr Phe His Pro Ala Asp Gly Leu Ser Leu Ile
125           450           455           460
126 Gly Gly Gly Arg Leu Gly His Tyr Lys Ile Glu Ser Gly Glu Gly Lys
127 465           470           475           480
128 Thr Leu His Lys Ala Ser Lys Thr Lys Phe Thr Gly Tyr Ala Gly Ala
129           485           490           495
130 Val Tyr Asp Leu Asn Asp Asn Asn Ser Leu Tyr Leu Ser Leu Ser Gln
131           500           505           510
132 Leu Tyr Thr Pro Gln Thr Asn Leu Asp Ala Asp Gly Lys Leu Leu Lys
133           515           520           525
134 Pro Arg Gln Gly Asn Gln Phe Glu Val Gly Tyr Lys Gly Ser Tyr Met
135           530           535           540
136 Asp Asp Arg Leu Asn Ala Arg Val Ser Phe Tyr Arg Met Lys Asp Lys
137 545           550           555           560
138 Asn Ala Ala Ala Pro Leu Asn Pro Asn Asn Lys Lys Thr Arg Tyr Ala
139           565           570           575
140 Ala Leu Gly Lys Arg Val Met Glu Gly Val Glu Thr Glu Ile Ser Gly
141           580           585           590
142 Ala Val Thr Pro Lys Trp Gln Ile His Ala Gly Tyr Ser Tyr Leu His
143           595           600           605
144 Ser Gln Ile Lys Thr Ala Ser Asn Ser Arg Asp Asp Gly Ile Phe Leu
145           610           615           620
146 Leu Met Pro Lys His Ser Ala Asn Leu Trp Thr Thr Tyr Gln Val Thr
147 625           630           635           640
148 Pro Glu Leu Thr Ile Gly Gly Gly Val Asn Ala Met Ser Gly Ile Thr
149           645           650           655
150 Ser Ser Ala Gly Met His Ala Gly Gly Tyr Ala Thr Phe Asp Ala Met
151           660           665           670
152 Ala Ala Tyr Arg Phe Thr Pro Lys Leu Lys Leu Gln Ile Asn Ala Asp
153           675           680           685
154 Asn Ile Phe Asn Arg His Tyr Tyr Ala Arg Val Gly Gly Ala Asn Thr
155           690           695           700
156 Phe Asn Ile Pro Gly Ser Glu Arg Thr Trp Thr Ala Asn Leu Arg Tyr

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157 705          710          715          720
158 Ser Phe
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 2078
163 <212> TYPE: DNA
164 <213> ORGANISM: Neisseria meningitidis
166 <400> SEQUENCE: 3
167 ccatggttg aaaccgtcac atcaaagggc agcgttcgta caacgcgatt gtcaccgaga      60
168 aaaacggcga ttacagctcg ttgcccgtca ccgtcggcac aaaaatcccc gcttctttgc      120
169 gcgaaattcc gcaatccgtc agtatcatca ccaaccagca ggtcaaagac cgcaatggtg      180
170 atacgtttga ccagttggcg cgcaaaacgc ccggcctgcg cgtgttgagc aacgatgacg      240
171 gacgctcttc ggtttacgcg cgcggttacg aatacagcga atacaacatc gacggcctgc      300
172 ccgcgcagat gcagagtatc aacggcacgc tgcccaatct gttcgccttc gaccgcgtgg      360
173 aagtgatgcg cgggcccagc ggactgttcg acagcagcgg cgagatgggc ggtatcgtga      420
174 atctggtgcg caaacgcccc accaaagcgt tccaaggtca tgctcgggca gggttcggta      480
175 cgcacaaaca atataaagcc gaggcggacg tatcgggcag cctcaattca gacggcagcg      540
176 tgcgcggccg cgtgatggcg cagaccgtcg gcgcgtctcc gcgtcccgcc gagaaaaaca      600
177 accggcacga aaccttctac gcggcggcgg attgggacat caaccccgat acggttttgg      660
178 gcgcgggcta tctttaccag caacgccacc tcgcgccgta caacggcttg ccagccgatg      720
179 ccaataacaa attaccgtcc ctgccgcaac acgtatttgt cggcgcggat tggaaacaaat      780
180 ttaaaatgaa cagccacgac gtgtttgcgg atttgaacaa ttacttcggc aacggcggct      840
181 acggcaaaagt cggtatgcgc tattccgacc gcgatgccga ctccaactat gcctttgccg      900
182 gcagcaagct gggcatgaaa accccggcag gccgccggg ctgcaatacg gctgacgaca      960
183 aagcctgcgc ggtgggtttg ggtacagaaa tcaaacaaaa agccctcgcg tttgacgcca      1020
184 gctacagcag gcctttccgc ttgggcaata cggccaacga atttgtcatc ggcgccgatt      1080
185 acaaccgctt ccgcagcacc aacgaacaag gccgtactac tttatatgca cgcggcggcc      1140
186 tggctttaaa cgagttccgc agcataccgc aggttgattt gattgccaac gcgcgcaaag      1200
187 gcgtgcgcgg ttacagccat accgtcgtca ccgaaaacct cgacgaattc ggcatttacg      1260
188 gcaaatccac cttccatcct gccgacgggc tgtcgcttat cggcggcgga cgtttgggac      1320
189 actataaaat cgagtcgggc gaaggcaaaa ccctgcacaa agccagcaaa accaagttca      1380
190 ccggctacgc aggcgcgggt tacgacttga acgacaacaa cagcctctac ctgagcctgt      1440
191 cccagctcta cacaccgcaa accaacctcg atgccgacgg caagctgctc aaaccgcgcc      1500
192 aaggcaacca gtttgaagtc ggttacaaaag gcagctacat ggacgaccgc ctcaatgccc      1560
193 gagtttcggt ctaccgcatg aaagacaaaa acgccgccgc accgttgaac ccgaacaaca      1620
194 aaaaaaccgc ttacgccgca ttgggcaaac gcgtgatgga aggcgttgag accgaaatca      1680
195 gcggcgcggg tacaccgaaa tggcaaatcc atgcaggtta cagctatctg cacagccaaa      1740
196 tcaaaaccgc ctccaattca cgcgacgacg gcatcttctt gctgatgccc aaacacagcg      1800
197 caaacctgtg gacgacttac caagttacgc ccgagctgac catcggcggc ggagtgaacg      1860
198 cgatgagcgg cattacttca tctgcaggga tgcagtcagg cgttatgcc acgttcgatg      1920
199 cgatggcgcg ataccgcttc acgcccaagc tgaagctgca aatcaacgcc gacaacatct      1980
200 tcaaccgcca ttactacgcc cgcgtcggcg gcgcgaacac cttaacatt cccggttcgg      2040
201 agcgcagcct gacggcaaac ctgcgttaca gtttttaa      2078
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 691
205 <212> TYPE: PRT
206 <213> ORGANISM: Neisseria meningitidis
208 <400> SEQUENCE: 4
209 Met Val Gly Asn Arg His Ile Lys Gly Gln Arg Ser Tyr Asn Ala Ile
210 1          5          10          15

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211 Val Thr Glu Lys Asn Gly Asp Tyr Ser Ser Phe Ala Val Thr Val Gly
212          20          25          30
213 Thr Lys Ile Pro Ala Ser Leu Arg Glu Ile Pro Gln Ser Val Ser Ile
214          35          40          45
215 Ile Thr Asn Gln Gln Val Lys Asp Arg Asn Val Asp Thr Phe Asp Gln
216          50          55          60
217 Leu Ala Arg Lys Thr Pro Gly Leu Arg Val Leu Ser Asn Asp Asp Gly
218 65          70          75          80
219 Arg Ser Ser Val Tyr Ala Arg Gly Tyr Glu Tyr Ser Glu Tyr Asn Ile
220          85          90          95
221 Asp Gly Leu Pro Ala Gln Met Gln Ser Ile Asn Gly Thr Leu Pro Asn
222          100         105         110
223 Leu Phe Ala Phe Asp Arg Val Glu Val Met Arg Gly Pro Ser Gly Leu
224          115         120         125
225 Phe Asp Ser Ser Gly Glu Met Gly Gly Ile Val Asn Leu Val Arg Lys
226          130         135         140
227 Arg Pro Thr Lys Ala Phe Gln Gly His Ala Ala Ala Gly Phe Gly Thr
228 145         150         155         160
229 His Lys Gln Tyr Lys Ala Glu Ala Asp Val Ser Gly Ser Leu Asn Ser
230          165         170         175
231 Asp Gly Ser Val Arg Gly Arg Val Met Ala Gln Thr Val Gly Ala Ser
232          180         185         190
233 Pro Arg Pro Ala Glu Lys Asn Asn Arg His Glu Thr Phe Tyr Ala Ala
234          195         200         205
235 Ala Asp Trp Asp Ile Asn Pro Asp Thr Val Leu Gly Ala Gly Tyr Leu
236          210         215         220
237 Tyr Gln Gln Arg His Leu Ala Pro Tyr Asn Gly Leu Pro Ala Asp Ala
238 225         230         235         240
239 Asn Asn Lys Leu Pro Ser Leu Pro Gln His Val Phe Val Gly Ala Asp
240          245         250         255
241 Trp Asn Lys Phe Lys Met Asn Ser His Asp Val Phe Ala Asp Leu Lys
242          260         265         270
243 His Tyr Phe Gly Asn Gly Gly Tyr Gly Lys Val Gly Met Arg Tyr Ser
244          275         280         285
245 Asp Arg Asp Ala Asp Ser Asn Tyr Ala Phe Ala Gly Ser Lys Leu Gly
246          290         295         300
247 Met Lys Thr Pro Ala Gly Arg Pro Gly Cys Asn Thr Ala Asp Asp Lys
248 305         310         315         320
249 Ala Cys Ala Val Gly Leu Gly Thr Glu Ile Lys Gln Lys Ala Leu Ala
250          325         330         335
251 Phe Asp Ala Ser Tyr Ser Arg Pro Phe Arg Leu Gly Asn Thr Ala Asn
252          340         345         350
253 Glu Phe Val Ile Gly Ala Asp Tyr Asn Arg Phe Arg Ser Thr Asn Glu
254          355         360         365
255 Gln Gly Arg Thr Thr Leu Tyr Ala Arg Gly Gly Leu Ala Leu Asn Glu
256          370         375         380
257 Phe Arg Ser Ile Pro Gln Val Asp Leu Ile Ala Asn Ala Arg Lys Gly
258 385         390         395         400
259 Val Arg Gly Tyr Ser His Thr Val Ala Thr Glu Asn Leu Asp Glu Phe

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VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date